LOCUS  EQE47250

```
  1  GGTTCCAGCTGCCGCGCACGCCCCGACCTTCCATCGTAGGCCGGACCATGGGAACCCCAAA   60
  1                                                  M  G  T  P  K    5

 61  GCCACGGNTCCTGCCCTGGCTGGTGTCGCAGCTGGGACCTGGGCAACTGGAGGGCGTGGC   120
  5   P  R  X  L  P  W  L  V  S  Q  L  G  Q  L  D  L  G  E  G  V  A   25

121  CTGGGTGAACAAGAGCCGCACGCGCTTCCGCATCCCTTGGAAGCACGGCCTACGGCAGGA   180
 25   W  V  N  K  S  R  T  R  F  R  I  P  W  K  H  G  L  R  Q  D   45

181  TGCACAGCAGGAGGATTTCGGAATCTTCCAGGCCTGGGCCGAGGCCACTGGTGCATATGT   240
 45   A  Q  Q  E  D  F  G  I  F  Q  A  W  A  E  A  T  G  A  Y  V   65

241  TCCCGGGAGGGATAAGCCAGACCTGCCAACCTGGAAGAGGAATTCCGCTCTGCCCTCAA   300
 65   P  G  R  D  K  P  D  L  P  T  W  K  R  N  F  R  S  A  L  N   85

301  CCGCAAAGAAGAGGGTTGCGTTTAGCAGAGACCGGAGCAAGGACCCTCACGACCCACATAA   360
 85   R  K  E  G  L  R  L  A  E  D  R  S  K  D  P  H  D  P  H  K   105

361  AATCTACGAGTTTGTGAACTCAGGAGTTGGGGACTTTTCCCAGCCAGACACCTCTCCGGA   420
105   I  Y  E  F  V  N  S  G  V  G  D  F  S  Q  P  D  T  S  P  D   125

421  CACCAATGGTGGAGGCAGTACTTCTGATACCCAGGAAGACATTCTGGATGAGTTACTGGG   480
125   T  N  G  G  G  S  T  S  D  T  Q  E  D  I  L  D  E  L  L  G   145
```

**Figure 1A**

```
481  TAACATGGTGTTGGCCCCACTCCCAGATCCCGGGACCCCCAGCCTGGCTGTAGCCCCTGA  540
145   N  M  V  L  A  P  L  P  D  P  G  P  P  S  L  A  V  A  P  E   165

541  GCCCTGCCCTCAGCCCCTGCGGAGCCCCAGCTTGGACAATCCACTCCCTTCCCAAACCT   600
165   P  C  P  Q  P  L  R  S  P  S  L  D  N  P  T  P  F  P  N  L   185

601  GGGGCCCTCTGAGAACCCACTGAAGCGGCTGTTGGTGCCGGGGGAAGAGTGGGAGTTCGA  660
185   G  P  S  E  N  P  L  K  R  L  L  V  P  G  E  E  W  E  F  E   205

661  GGTGACAGCCTTCTACCGGGGCCGCCAAGTCTTCCAGCAGACCATCTCCTGCCCGGAGGG  720
205   V  T  A  F  Y  R  G  R  Q  V  F  Q  Q  T  I  S  C  P  E  G   225

721  CCTGCGGGCTGGTGGGGTCCGAAGTGGGAGACAGGACGCTGCCTGGATGGCCAGTCACACT  780
225   L  R  L  V  G  S  E  V  G  D  R  T  L  P  G  W  P  V  T  L   245

781  GCCAGACCCTGGCATGTCCCTGACAGACAGGGGAGTGATGAGCTACGTGAGGCATGTGCT  840
245   P  D  P  G  M  S  L  T  D  R  G  V  M  S  Y  V  R  H  V  L   265

841  GAGCTGCCTGGGTGGGGGACTGGCTCTCTGGGCCGGGCCAGTGGCTCTGGGCCCCAGCG   900
265   S  C  L  G  G  G  L  A  L  W  R  A  G  Q  W  L  W  A  Q  R   285

901  GCTGGGGGCACTGCCACACATACTGGGCAGTGAGCGAGGAGCTGCTCCCCAACAGCGGGCA  960
285   L  G  H  C  H  T  Y  W  A  V  S  E  E  L  L  P  N  S  G  H   305
```

**Figure 1B**

```
 961  TGGGCCTGATGGGCCGAGGTCCCCAAGGACAAGGAAGGAGGCGGTGTTGACCTGGGGCCCTT  1020
 305   G   P   D   G   E   V   P   K   D   K   E   G   G   V   F   D   L   G   P   F   325

1021  CATTGTAGATCTGATTACCTTCACGGAAGGAAGCGGACGCTCACCACGCTATGCCCTCTG  1080
 325   I   V   D   L   I   T   F   T   E   G   S   G   R   S   P   R   Y   A   L   W   345

1081  GTTCTGTGTGGGGGAGTCATGGCCCCAGGACCAGCCGTGGACCAAGAGGCTCGTGATGGT  1140
 345   F   C   V   G   E   S   W   P   Q   D   Q   P   W   T   K   R   L   V   M   V   365

1141  CAAGGTTGTGCCCACGTGCCTCAGGGCCTTGGTAGAAATGGCCCGGGTAGGGGGTGCCTC  1200
 365   K   V   V   P   T   C   L   R   A   L   V   E   M   A   R   V   G   G   A   S   385

1201  CTCCCCTGGAGAATACTGTGGACCTGCACATTCCAACAGCCACCACTCTCCCTCACCTC  1260
 385   S   L   E   N   T   V   D   L   H   I   S   N   S   H   P   L   S   L   T   S   405

1261  CGACCAGTACAAGGCCTACCTGCGAGGACTTGGTGGAGGGCATGGATTTCCAGGGCCCTGG  1320
 405   D   Q   Y   K   A   Y   L   Q   D   L   V   E   G   M   D   F   Q   G   P   G   425

1321  GGAGAGCTGAGCCCCTGCGCTCCTCATGGTGTGTGCCTCCAACCCCCCTGTTCCCCACCACCTC  1380
 425   E   S   *   427

1381  AACCAATAAACTGGTTCCTGCTATGAAAAAAAAAAAAAAAAAAAA  1426
```
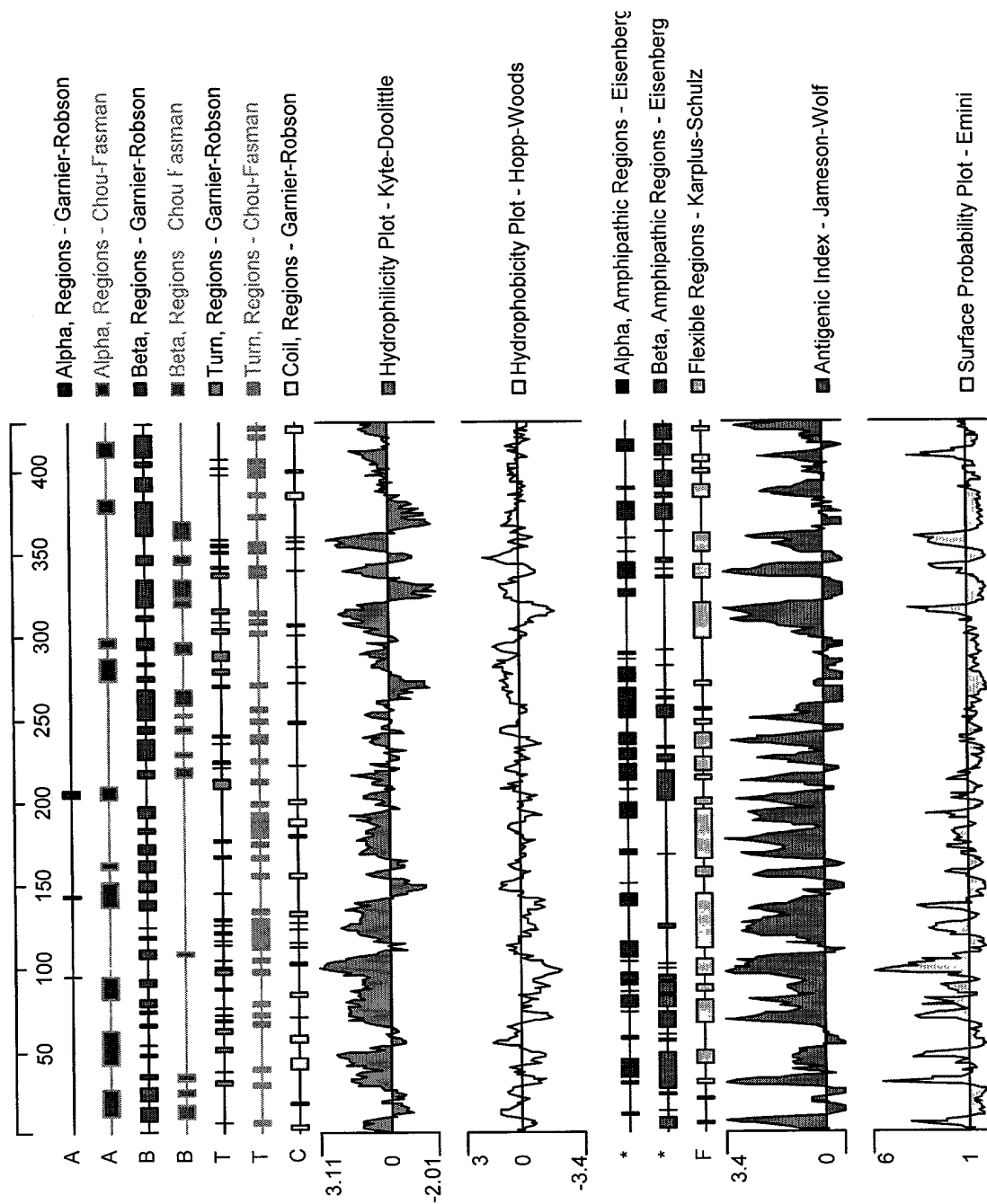
**Figure 1C**

Figure 2